RAW SEQUENCE LISTING

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Application Serial Number: _10/518,884_

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RAW SEQUENCE LISTING   DATE: 03/03/2006
PATENT APPLICATION: **US/10/518,884**   TIME: 12:57:49

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 3 <110> APPLICANT: Martin, Catherine R
 4        Michael, Anthony
 5        Niggeweg, Ricarda
 7 <120> TITLE OF INVENTION: Plant-Derived Transferase Genes
 9 <130> FILE REFERENCE: 0380-P03542US0
11 <140> CURRENT APPLICATION NUMBER: US 10/518,884
12 <141> CURRENT FILING DATE: 2004-12-20
14 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/002645
15 <151> PRIOR FILING DATE: 2003-06-17
17 <150> PRIOR APPLICATION NUMBER: GB 0214406.1
18 <151> PRIOR FILING DATE: 2002-06-21
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn version 3.1
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26 <212> TYPE: PRT
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39 Leu Asp Leu Ile Val Gly Arg Ile His Leu Leu Thr Val Tyr Phe Tyr
40         35                  40                  45
43 Lys Pro Asn Gly Ser Ser Asn Phe Phe Asp Asn Lys Val Ile Lys Glu
44     50                  55                  60
47 Ala Leu Ser Asn Val Leu Val Ser Phe Tyr Pro Met Ala Gly Arg Leu
48 65                  70                  75                  80
51 Gly Arg Asp Glu Gln Gly Arg Ile Glu Val Asn Cys Asn Gly Glu Gly
52             85                  90                  95
55 Val Leu Phe Val Glu Ala Glu Ser Asp Ser Cys Val Asp Asp Phe Gly
56             100                 105                 110
59 Asp Phe Thr Pro Ser Leu Glu Leu Arg Lys Leu Ile Pro Ser Val Glu
60         115                 120                 125
63 Thr Ser Gly Asp Ile Ser Thr Phe Pro Leu Val Ile Phe Gln Ile Thr
64     130                 135                 140
67 Arg Phe Lys Cys Gly Gly Val Ala Leu Gly Gly Gly Val Phe His Thr
68 145                 150                 155                 160
71 Leu Ser Asp Gly Leu Ser Ser Ile His Phe Ile Asn Thr Trp Ser Asp
72             165                 170                 175
75 Ile Ala Arg Gly Leu Ser Val Ala Val Pro Pro Phe Ile Asp Arg Thr
76             180                 185                 190
79 Leu Leu Arg Ala Arg Asp Pro Pro Thr Tyr Ser Phe Glu His Val Glu
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80          195               200               205
83 Tyr His Pro Pro Pro Thr Leu Asn Ser Ser Lys Asn Arg Glu Ser Ser
84      210               215               220
87 Thr Thr Thr Met Leu Lys Phe Ser Ser Glu Gln Leu Gly Leu Leu Lys
88 225               230               235               240
91 Ser Lys Ser Lys Asn Glu Gly Ser Thr Tyr Glu Ile Leu Ala Ala His
92               245               250               255
95 Ile Trp Arg Cys Thr Cys Lys Ala Arg Gly Leu Pro Glu Asp Gln Leu
96               260               265               270
99 Thr Lys Leu His Val Ala Thr Asp Gly Arg Ser Arg Leu Cys Pro Pro
100          275               280               285
103 Leu Pro Pro Gly Tyr Leu Gly Asn Val Val Phe Thr Ala Thr Pro Ile
104      290               295               300
107 Ala Lys Ser Cys Glu Leu Gln Ser Glu Pro Leu Thr Asn Ser Val Lys
108 305               310               315               320
111 Arg Ile His Asn Glu Leu Ile Lys Met Asp Asp Asn Tyr Leu Arg Ser
112               325               330               335
115 Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Thr Leu Ile Arg
116               340               345               350
119 Gly Pro Ala Tyr Phe Ala Ser Pro Asn Leu Asn Ile Asn Ser Trp Thr
120      355               360               365
123 Arg Leu Pro Val His Glu Cys Asp Phe Gly Trp Gly Arg Pro Ile His
124      370               375               380
127 Met Gly Pro Ala Cys Ile Leu Tyr Glu Gly Thr Ile Tyr Ile Ile Pro
128 385               390               395               400
131 Ser Pro Asn Ser Lys Asp Arg Asn Leu Arg Leu Ala Val Cys Leu Asp
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135 Ala Gly His Met Ser Leu Phe Glu Lys Tyr Leu Tyr Glu Leu
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151               20               25               30
154 Leu Asp Leu Ile Val Gly Arg Ile His Leu Leu Thr Val Tyr Phe Tyr
155      35               40               45
158 Lys Pro Asn Gly Ser Ser Asn Phe Phe Asp Ser Lys Ile Met Lys Glu
159      50               55               60
162 Ala Leu Ser Asn Val Leu Val Ser Phe Tyr Pro Met Ala Gly Arg Leu
163 65               70               75               80
166 Ala Arg Asp Glu Gln Gly Arg Ile Glu Ile Asn Cys Asn Gly Glu Gly
167               85               90               95
170 Val Leu Phe Val Glu Ala Glu Ser Asp Ala Phe Val Asp Asp Phe Gly
171               100               105               110
174 Asp Phe Thr Pro Ser Leu Glu Leu Arg Lys Leu Ile Pro Thr Val Asp
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175          115                   120                    125
178 Thr Ser Gly Asp Ile Ser Thr Phe Pro Leu Ile Ile Phe Gln Val Thr
179     130                   135                    140
182 Arg Phe Lys Cys Gly Gly Val Ser Leu Gly Gly Gly Val Phe His Thr
183 145                   150                   155                    160
186 Leu Ser Asp Gly Leu Ser Ser Ile His Phe Ile Asn Thr Trp Ser Asp
187                   165                   170                   175
190 Ile Ala Arg Gly Leu Ser Val Ala Ile Pro Pro Phe Ile Asp Arg Thr
191             180                   185                   190
194 Leu Leu Arg Ala Arg Asp Pro Pro Thr Ser Ser Phe Glu His Val Glu
195         195                   200                   205
198 Tyr His Pro Pro Pro Ser Leu Ile Ser Ser Ser Lys Ser Leu Glu Ser
199     210                   215                   220
202 Thr Ser Pro Lys Pro Ser Thr Thr Thr Met Leu Lys Phe Ser Ser Asp
203 225                   230                   235                    240
206 Gln Leu Gly Leu Leu Lys Ser Lys Ser Lys His Asp Gly Ser Thr Tyr
207                   245                   250                   255
210 Glu Ile Leu Ala Ala His Ile Trp Arg Cys Thr Cys Lys Ala Arg Ala
211             260                   265                   270
214 Leu Ser Asp Asp Gln Leu Thr Lys Leu His Val Ala Thr Asp Gly Arg
215         275                   280                   285
218 Ser Arg Leu Cys Pro Pro Leu Pro Pro Gly Tyr Leu Gly Asn Val Val
219     290                   295                   300
222 Phe Thr Gly Thr Pro Met Ala Lys Ser Ser Glu Leu Leu Gln Glu Pro
223 305                   310                   315                    320
226 Leu Thr Asn Ser Ala Lys Arg Ile His Ser Ala Leu Ser Lys Met Asp
227                   325                   330                   335
230 Asp Asn Tyr Leu Arg Ser Ala Leu Asp Tyr Leu Glu Leu Leu Pro Asp
231                   340                   345                   350
234 Leu Ser Ala Leu Ile Arg Gly Pro Thr Tyr Phe Ala Ser Pro Asn Leu
235         355                   360                   365
238 Asn Ile Asn Ser Trp Thr Arg Leu Pro Val His Asp Ser Asp Phe Gly
239     370                   375                   380
242 Trp Gly Arg Pro Ile His Met Gly Pro Ala Cys Ile Leu Tyr Glu Gly
243 385                   390                   395                    400
246 Thr Val Tyr Ile Leu Pro Ser Pro Asn Ser Lys Asp Arg Asn Leu Arg
247                   405                   410                   415
250 Leu Ala Val Cys Leu Asp Ala Asp His Met Pro Leu Phe Glu Lys Tyr
251             420                   425                   430
254 Leu Tyr Glu Phe
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260 <212> TYPE: DNA
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266 aaaccaacac caacaaaaag actttggagt tctaacttag atttaatagt gggaagaatt      120
268 catcttttaa cagtatattt ctataaacca aatggatctt caaatttctt tgattcaaaa      180
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270 ataatgaaag aagcattaag taatgttctt gtttcatttt acccaatggc tggaagatta  240
272 gctagagatg aacaaggaag aattgagata aattgtaatg gagaaggagt tttatttgtt  300
274 gaagctgaaa gtgatgcttt tgttgatgat tttggtgatt ttactccaag tttggaactt  360
276 aggaaactta ttcctactgt tgacacttct ggtgatattt ctactttccc cctcatcatc  420
278 tttcaggtta ctcgtttcaa atgtggtgga gtttcacttg gtggaggagt attccacact  480
280 ttatcagatg gtctctcatc aattcacttc atcaacacat ggtccgatat agcccgaggc  540
282 ctctccgtcg ccatcccgcc gttcatcgac cggaccctcc tccgtgcacg ggacccacca  600
284 acatcgtctt tcgagcacgt cgagtatcat cctcctccat ctctaatttc atcatcaaaa  660
286 agcttagaat ccactagccc aaagcctagt accacaacca tgttaaaatt ctctagtgac  720
288 caacttgggc ttctaaagtc caagtccaaa catgatggta gcacttacga aatcctcgcg  780
290 gcccatattt ggcgttgcac gtgcaaggca cgtgcactgt ccgacgatca attgaccaaa  840
292 ttacatgtgg ccactgatgg taggtctagg ctttgccctc ctttgccacc aggttactta  900
294 ggaaatgttg tgttcacagg cacacctatg gcaaaatcaa gtgaactttt acaagaacca  960
296 ttgacaaatt cagccaagag aattcatagt gcattatcaa aaatggatga caattaccta 1020
298 agatcagctc tcgattacct cgaattactg cccgatttat cggctttaat ccgtggaccg 1080
300 acgtactttg ctagccctaa tcttaatatt aatagttgga ctagattgcc tgttcatgat 1140
302 tcagattttg gatggggaag gccaattcat atgggaccag cttgcatttt atatgaaggg 1200
304 acagtttata tattgccaag tccaaatagt aaagatagga acttgcgttt ggctgtttgt. 1260
306 ttagatgctg atcacatgcc act.ttgag aagtatttgt atgaattttg agaggttgaa 1320
308 aaaaaaatca agaatgttcc aacacttgag aattatctta ggtgtgggtg gtttttggatt 1380
310 aaggcatttt gtaacttgtt ttctattgtt tttttggggg gtcagtttgt tttcaaaaaa 1440
312 aaaaaaaaaa aaaaaa                                                   1456
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316 <211> LENGTH: 1293
317 <212> TYPE: DNA
318 <213> ORGANISM: Lycopersicon esculentum
320 <400> SEQUENCE: 4
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323 aaaccaacac caacaaagag aatttggagt tctaatttgg atttaattgt tggaagaatt   120
325 catcttttga ctgtttattt ttataaacca aatggatctt caaatttttt tgataataaa   180
327 gttattaaag aagcattaag taatgtttta gtttcatttt atccaatggc tggaagatta   240
329 ggtagggatg aacaaggtag aattgaagtt aattgtaatg gtgaaggtgt tttgtttgtt   300
331 gaggctgaaa gtgattcatg tgttgatgat tttggtgatt ttacaccatc tttggaactt   360
333 agaaaactca ttccaagtgt tgaaacctct ggagatatct caactttccc actagttata   420
335 tttcagatta ctcgtttcaa gtgtggcgga gtcgctcttg gtggtggagt attccacacg   480
337 ttatccgatg gtctctcatc catccacttc atcaacacgt ggtcggacat cgcccgtggc   540
339 ctctccgtcg cagtcccgcc gttcatcgat cggacgctcc tccgtgcaag ggacccaccg   600
341 acatattctt tcgagcacgt tgagtaccat cctccaccta ccctaaactc atcgaaaat   660
343 cgcgagtcca gtaccacgac catgttgaaa ttctcgagtg aacaactcgg gcttcttaag   720
345 tccaagtcca aaaatgaggg tagcacctat gaaatcctcg cagcccatat ttggcgatgc   780
347 acgtgcaagg cacgtggatt gccagaggat caattgacca aattacacgt ggccaccgac   840
349 ggaaggtcaa ggctttgccc tcccttgcca ccgggttacc taggaaacgt cgtgttcacg   900
351 gcaaccccaa tagctaaatc atgcgaactt caatcagagc cgttgacaaa ttccgtcaag   960
353 agaattcaca acgagttgat caaaatggac gacaattacc taagatcagc actggattac  1020
355 ctcgaattac aacctgattt atcaacccta attcggggcc cggcttactt tgctagccct  1080
357 aacctcaata ttaatagttg gactaggttg cctgtccatg agtgtgattt ggatggggt  1140
359 aggccaattc atatgggacc agcttgcatt ttatatgaag ggacaattta tattatacca  1200
361 agtccaaatt ctaaagatag gaacttgcgt ttggctgttt gtctagatgc tggtcacatg  1260
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369 <213> ORGANISM: Artificial sequence
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416 <212> TYPE: DNA
417 <213> ORGANISM: Artificial sequence
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/518,884**

DATE: 03/03/2006
TIME: 12:57:50

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